

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 13:46:59 ; Search time 15 Seconds

(without alignments)
83.366 Million cell updates/sec

Title: US-09-674-616A-2

Sequence: 1 NQGVSPYTLKG 13

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 246

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	29.9	13	2 S47361	T-cell antigen rec
2	20	29.9	13	2 B56864	dipeptidyl-peptida
3	19	28.4	13	2 S32473	lymadFamide 3 - g
4	19	28.4	13	2 PL0157	Ig kappa chain V-I
5	18	26.9	13	2 B61458	Ig kappa chain V-I
6	18	26.9	13	2 A61458	Ig kappa chain V-I
7	17	25.4	13	1 UNBO	neurotensin - bovi
8	17	25.4	13	2 A44818	neurotensin - bovi
9	17	25.4	13	2 A53608	extracellular lipa
10	17	25.4	13	2 A28505	neurotensin - guin
11	17	25.4	13	2 A61067	neurotensin [valid
12	17	25.4	13	2 A05174	neurotensin - comm
13	17	25.4	13	2 PT0256	tryptophyltin-13 -
14	16	23.9	13	2 PC1149	Ig heavy chain CRD
15	16	23.9	13	2 A61514	equinacoxin 1A - s
16	15	22.4	13	2 S15755	glutathione transf
17	15	22.4	13	2 B26093	actin 7 - soybean
18	15	22.4	13	2 A54326	microbial collagen
19	15	22.4	13	2 B28810	glutathione transf
20	15	22.4	13	2 S47358	glutathione transf
21	15	22.4	13	2 PH1599	Ig H chain V-D-J r
22	14	20.9	13	2 A61361	bradykinin-like pe
23	14	20.9	13	2 PU0038	alpha-peptide/angi
24	14	20.9	13	2 S36668	hypothetical prote
25	14	20.9	13	2 S32471	lymadFamide 1 - g
26	14	20.9	13	2 S32472	lymadFamide 2 - g
27	14	20.9	13	2 D61458	Ig kappa chain V-I
28	14	20.9	13	2 E61458	Ig kappa chain V-I
29	14	20.9	13	2 S47362	T-cell antigen rec

30	14	20.9	13	2 S47380	T-cell antigen rec
31	14	20.9	13	2 B61233	concepcus protein
32	14	20.9	13	2 PH1595	Ig H chain V-D-J r
33	14	20.9	13	2 PH0786	T-cell receptor al
34	14	20.9	13	2 151905	collecting duct wa
35	13	19.4	13	2 S39413	tubulin beta chain
36	13	19.4	13	2 A32453	phloroglucinol red
37	13	19.4	13	2 S36887	ribosomal protein
38	13	19.4	13	2 PH0138	T-cell receptor be
39	13	19.4	13	2 B47415	mannose-1-phosphat
40	13	19.4	13	2 G37256	Ig heavy chain C r
41	13	19.4	13	2 D37267	Ig heavy chain C r
42	13	19.4	13	2 C47630	Ig kappa chain J r
43	13	19.4	13	2 G83968	hypothetical prote
44	13	19.4	13	2 H85575	hypothetical prote
45	13	19.4	13	2 A59491	epithelial dog all

ALIGNMENTS

RESULT 1
S47361
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47361
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47355
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35685; NID:G527459; PIDN:CAA84754.1; PID:G527460
C/Keywords: T-cell receptor

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVSPY 8
DB 5 QGSPY 9

RESULT 2
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C/Accession: B56864
R/Plakidou-Dymock, S.; McGivan, J.D.
Biochim. Biophys. Acta 1145, 105-112, 1993
A/Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border mem
A/Reference number: A56864; PMID:93136203; PMID:8093655
A/Accession: B56864
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <PLA>
A/Experimental source: renal brush-border membrane vesicles
C/Keywords: dipeptidylpeptide hydrolase

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.6e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 SPYTLKG 13
DB 3 TPWKVLSG 10

RESULT 3

S32473

LymnadPamide 3 - great pond snail

C:Species: Lymnaea stagnalis (great pond snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

C:Accession: S32473

R:Uhmssen, A.H.; Rehfeld, J.F.

Eur. J. Biochem. 213, 875-879, 1993

A:Title: LymnadPamides, a new family of neuropeptides from the pond snail, Lymnaea stagnalis

A:Reference number: S32471; MUID:93238777; PMID:8477756

A:Accession: S32473

A:Molecule type: protein

A:Residues: 1-13 <JOB>

A:Cross-references: PDB:AA26364.1; PID:g299831

A:Experimental source: ganglia

C:Keywords: amidated carboxyl end; neuropeptide

F:1/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 2.4e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PYTLKG 13

Db 1 PYDRISG 7

RESULT 4

P10157

Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997

C:Accession: P10157; C61458

R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A:Title: Expression of a public idioType by human monoclonal IGM directed to myelin-assoc

A:Reference number: A61458; MUID:90039128; PMID:2478651

A:Accession: P10157

A:Molecule type: protein

A:Residues: 1-13 <BRO>

A:Accession: C61458

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BR2>

C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycop

C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 28.4%; Score 19; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPYTL 10

Db 7 SPYTL 11

RESULT 5

B61458

Ig kappa chain V-I region (BLA) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996

C:Accession: B61458

R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A:Title: Expression of a public idioType by human monoclonal IGM directed to myelin-assoc

A:Reference number: A61458; MUID:90039128; PMID:2478651

A:Accession: B61458

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BRO>

C:Keywords: heterotetramer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPYTL 10

Db 7 SPYTL 11

RESULT 6

A61458

Ig kappa chain V-I region (BOU) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996

C:Accession: A61458; P10156

R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A:Title: Expression of a public idioType by human monoclonal IGM directed to myelin-assoc

A:Reference number: A61458; MUID:90039128; PMID:2478651

A:Accession: A61458

A:Molecule type: protein

A:Residues: 1-13 <BRO>

C:Comment: This protein is one of monoclonal IGM reactive with myeloma-associated glycop

C:Keywords: heterotetramer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPYTL 10

Db 7 SPYTL 11

RESULT 7

U080

neurotensin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995

C:Accession: A01420

R:Carraway, R.; Leeman, S.E.

J. Biol. Chem. 250, 1907-1911, 1975

A:Title: The amino acid sequence of a hypothalamic peptide, neurotensin.

A:Reference number: A92172; MUID:75095678; PMID:1167549

A:Accession: A01420

A:Molecule type: protein

A:Residues: 1-13 <CAR>

A:Experimental source: hypothalamus

R:Carraway, R.; Leeman, S.E.

J. Biol. Chem. 250, 1912-1918, 1975

A:Title: The synthesis of neurotensin.

A:Reference number: A92173; MUID:75095679; PMID:1112838

A:Contents: annotation; synthesis

A>Note: a tridecapeptide chemically and pharmacologically identical with the natural pep

C:Keywords: neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 1; Length 13;

Best Local Similarity 75.0%; Pred. No. 5.9e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10

Db 10 PYTL 13

RESULT 8

A44818

extracellular lipase - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa

C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C:Accession: A44818

R:Gilbert, E.J.; Cornish, A.; Jones, C.W.

J. Gen. Microbiol. 137, 2223-2229, 1991
 A>Title: Purification and properties of extracellular lipase from *Pseudomonas aeruginosa*
 A:Reference number: A44818; MUID:92085040; PMID:1748875
 A:Accession: A44818
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-13 <GIL>
 A:Experimental source: strain TE3285
 A>Note: sequence extracted from NCBI backbone (NCBI:70395)
 C:Superfamily: Pseudomonas triacylglycerol lipase

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 5.9e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 SPYTLK 12
 |||
 1 STYQTK 7

RESULT 9

A53608
 neurotensin - guinea pig
 C:Species: *Cavia porcellus* (guinea pig)
 C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Sep-2000
 C:Accession: A53608
 R:Shaw, C.; Thim, L.; Conlon, J.M.
 FEBS Lett. 202, 187-191, 1986
 A>Title: [Ser(7)]neurotensin: isolation from guinea pig intestine.
 A:Reference number: A53608; MUID:86248085; PMID:3087775
 A:Accession: A53608
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <SHA>
 C:Superfamily: neurotensin
 C:Keywords: neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
 |||
 10 PYTL 13

RESULT 10

A28505
 neurotensin [validated] - chicken
 C:Species: *Gallus gallus* (chicken)
 C>Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: A28505
 R:Iwabuchi, H.; Komori, S.; Ohashi, H.; Kimura, S.
 Jpn. J. Pharmacol. 44, 455-459, 1987
 A>Title: The amino acid sequence of a smooth muscle-contracting peptide from chicken rectum
 A:Reference number: A28505; MUID:88063566; PMID:3682409
 A:Accession: A28505
 A:Molecule type: protein
 A:Residues: 1-13 <IWA>
 A:Experimental source: rectum
 C:Comment: The peptide isolated from rectum is identical with chicken neurotensin and has
 C:Superfamily: neurotensin
 C:Keywords: hormone; neuropeptide; pyroglutamic acid
 F:1-13/Product: neurotensin #status experimental <NTS>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
 |||

DB 10 PYTL 13

RESULT 11

A61067
 neurotensin - common frog
 C:Species: *Rana temporaria* (common frog)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Aug-1994
 C:Accession: A61067
 R:Shaw, C.; McKay, D.M.; Halton, D.W.; Thim, L.; Buchanan, K.D.
 Regul. Pept. 38, 23-31, 1992
 A>Title: Isolation and primary structure of an amphibian neurotensin.
 A:Reference number: A61067; MUID:92245104; PMID:1574601
 A:Accession: A61067
 A:Molecule type: protein
 A:Residues: 1-13 <SHA>
 A>Note: this peptide was identified in brain, intestine, and rectum, but not in stomach
 C:Superfamily: neurotensin
 C:Keywords: brain; intestine; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
 |||
 10 PYTL 13

RESULT 12

A05174
 tryptophyllin-13 - Rohde's leaf frog
 C:Species: *Phyllomedusa rohdei* (Rohde's leaf frog)
 C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
 C:Accession: A05174
 R:Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
 Int. J. Pept. Protein Res. 27, 175-182, 1986
 A:Reference number: A05174
 A:Accession: A05174
 A:Molecule type: protein
 A:Residues: 1-13 <MON>
 C:Superfamily: unassigned animal peptides
 C:Keywords: pyroglutamic acid; skin
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 QVSPY 8
 |||
 1 QKPY 5

RESULT 13

PT0256
 Ig heavy chain CDR3 region (clone 2-115C) - human (fragment)
 C:Species: *Homo sapiens* (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0256
 R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and junctional diversity in the CDR3 region of the heavy chain of a human anti-lymphocyte antigen (CD45) monoclonal antibody
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0256
 A:Molecule type: DNA
 A:Residues: 1-13 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 5.9e+03;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YTLKLG 13
| : ||
Db 4 YDMLTG 9

RESULT 14

PC1149
equinatoxin 1A - sea anemone (Actinia equina) (fragment)
C:Species: Actinia equina
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PC1149
R:Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
Chem. Pharm. Bull. 40, 2873-2875, 1992
A:Title: Isolation and characterization of equinatoxins from the sea anemone Actinia equina
A:Reference number: PC1149; MUID:93099631; PMID:1361161
A:Accession: PC1149
A:Molecule type: protein
A:Residues: 1-13 <KOM>
C:Keywords: toxin

Query Match 23.9%; Score 16; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOEQV 5
| : ||
Db 4 NOAEV 8

RESULT 15

A61514
glutathione transferase (EC 2.5.1.18), 26k - fluke (Schistosoma japonicum) (fragment)
C:Species: Schistosoma japonicum
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 07-May-1999
C:Accession: A61514
R:Mitchell, G.F.
Mol. Biochem. Parasitol. 27, 249-256, 1988
A:Title: Expression of an enzymatically active parasite molecule in Escherichia coli: Schistosoma japonicum
A:Reference number: A61514; MUID:88142994; PMID:3278228
A:Accession: A61514
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <MIT>
C:Keywords: transferase

Query Match 23.9%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YTLKLG 13
| : ||
Db 6 YWKIKG 11

Search completed: October 1, 2004, 13:48:33
Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 13:46:58 ; Search time 9 Seconds

(without alignments)
75.212 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67

Sequence: 1 NQEQVSPYTLK 13

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 96

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	29.9	13	1	IDHA CANFA
2	19	28.4	13	1	CHEP PARID
3	19	28.4	13	1	NP3 LYMS
4	18	26.9	13	1	FR12 PRA
5	17	25.4	13	1	NEUT BUPMA
6	17	25.4	13	1	NEUT CAPVO
7	17	25.4	13	1	NEUT CHICK
8	17	25.4	13	1	NEUT RANTE
9	17	25.4	13	1	TY13 PHYRO
10	16	23.9	13	1	PEDI HYDAT
11	16	23.9	13	1	PROX ORYSA
12	16	23.9	13	1	SA2B ONCMY
13	16	23.9	13	1	SA2B ONCMY
14	15	22.4	13	1	ACT7 SOYBN
15	15	22.4	13	1	E121 LITRU
16	15	22.4	13	1	E122 LITRU
17	15	22.4	13	1	UN12 CLOPA
18	15	22.4	13	1	UN1 UPEIN
19	14	20.9	13	1	BRK PARID
20	14	20.9	13	1	CRBL VESMA
21	14	20.9	13	1	MPI MICOC
22	14	20.9	13	1	NP1 LYMS
23	14	20.9	13	1	NP2 LYMS
24	14	20.9	13	1	SODM CANFA
25	14	20.9	13	1	TEWC RANTE
26	14	20.9	13	1	YEP2 LACLC
27	13	19.4	13	1	FIIB RABIT
28	13	19.4	13	1	PHGR EUBOX
29	13	19.4	13	1	UN10 CLOPA
30	12	17.9	13	1	CRBL VESAN
31	12	17.9	13	1	CRBL VESCR
32	12	17.9	13	1	CRBL VESXA
33	12	17.9	13	1	PSAE_PEA

34	12	17.9	13	1	PSAU PEA	P17229	pisum sativ
35	12	17.9	13	1	UHA3 CANFA	P56535	canis fam1
36	12	17.9	13	1	VGL6 BACSU	P80867	bacillus su
37	11	16.4	13	1	AUI1 LITRA	P82366	litorea ran
38	11	16.4	13	1	AUI2 LITRA	P82367	litorea ran
39	11	16.4	13	1	BPPI BOTJA	P01020	bothrops ja
40	11	16.4	13	1	CRBL ICASP	P17237	icaria sp.
41	11	16.4	13	1	CRBL VESLE	P17235	vespula lew
42	11	16.4	13	1	CRTC BOVIN	P28489	bos taurus
43	11	16.4	13	1	CRTC RANES	P31832	rana esculen
44	11	16.4	13	1	EP65 HUMAN	P54963	homo sapien
45	11	16.4	13	1	GER1 HORVU	P28525	hordeum vul

ALIGNMENTS

RESULT 1

IDHA CANFA STANDARD; PRT; 13 AA.

AC P54836; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-0UL-1998 (Rel. 36, Last annotation update)

DE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial

DE (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD+-specific ICDH)

DE (Fragment).

GN IDH3A.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE.

RC TISSUE=Heart;

RX MEDLINE=98163340; PubMed=9504812;

RA Dunn M.J., Corbett J.M., Wheeler C.H.;

RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of

dog heart proteins."

RL Electrophoresis 18:2795-2802 (1997).

CC -1- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) +

NADH.

CC -1- SUBUNIT: Heterooligomer of subunits alpha, beta, and gamma in the

CC -1- SUBCELLULAR LOCATION: Mitochondrial

CC -1- SIMILARITY: Belongs to the isocitrate and isopropylmalate

CC dehydrogenases family.

DR HSC-2DPAGE; P54836; DOG.

DR InterPro; IPR001804; Isoch.

DR PROSITE; PS00470; IDH IMDH; PARTIAL.

KW Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.

FT NON TER

SQ SEQUENCE 13 AA; 1356 MW; 9ABFBC2B2A34B2D1 CRC64;

QY 4 QVSPYTLK 13

Db 3 EVQVTLIPG 12

RESULT 2

CHEP PARID STANDARD; PRT; 13 AA.

AC P42718; 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Chemotactic peptide.

OS Parapolybia indica.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespiidae; Polistinae; Parapolybia.
 OX NCBI_TaxID=31921;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Toki T., Yasuhara T., Nakajima T.;
 RT "Isolation and sequential analysis of peptides on the venom sac of
 Parapolybia indica.";
 RL Bisel Dobutau 39:105-111(1988).
 KW Chemotaxis; Amidation.
 FT MOD RES 13 13
 SQ SEQUENCE 13 AA; 1298 MW; 5C950CE8E39D5873 CRC64;
 QY Query Match 28.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 10 LKMG 13
 4 LKMG 7

RESULT 3
 NP3_LYMWST STANDARD; PRT; 13 AA.
 AC P80180;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Lyman-DF-amide 3.
 OS Lymanaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymanaeoidea; Lymanaeidae; Lymanaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=9328777; PubMed=8477756;
 RA Johnson A.H., Rehfeld J.F.;
 RT "LymanadFamides, a new family of neuropeptides from the pond snail,
 Lymanaea stagnalis. Clue to cholecystokinin immunoreactivity in
 invertebrates?";
 RL But. J. Biochem. 213:875-879(1993).
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
 DR PIR; S32473; S32473.
 KW Neuropeptide; Amidation.
 FT MOD RES 13 13
 FT UNSURE 12 12
 SQ SEQUENCE 13 AA; 1462 MW; 9CA07BAF5D5B865 CRC64;
 QY Query Match 28.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Db 7 PYTLKG 13
 1 PYDRISG 7

RESULT 4
 FR12_PEA STANDARD; PRT; 13 AA.
 AC P83445;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ferritin 2, chloroplast (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3886;

RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC STRAIN=cv. Laxton's Progress; TISSUE=leaf;
 RA Shingler R., McCarty R.E.;
 RL Submitted (SEP-2002) to Swiss-Prot.
 CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
 in a soluble, nontoxic, readily available form. The functional and
 molecule, which is composed of 24 chains, is roughly spherical and
 contains a central cavity into which the polymeric ferric iron
 core is deposited.
 CC -1- SUBCELLULAR LOCATION: Chloroplast (inner envelope membrane), and
 other plastids.
 CC -1- TISSUE SPECIFICITY: Leaves.
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
 4.74, its MW is: 25.7 kDa.
 CC -1- SIMILARITY: Belongs to the ferritin family.
 DR InterPro: IPR001519; Ferritin.
 DR InterPro: IPR009040; Ferritin-like.
 DR PROSITE: PS00204; FERRITIN_2; PARTIAL.
 DR PROSITE: PS00540; FERRITIN_1; PARTIAL.
 DR PROSITE: PS50905; FERRITIN-LIKE; PARTIAL.
 KW Iron storage; Iron; Metal-binding; Chloroplast.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1246 MW; 26C9DC25F34ADC7 CRC64;
 QY Query Match 26.3%; Score 18; DB 1; Length 13;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 6 SPYTL 10
 5 SPATL 9

RESULT 5
 NEUT_BUPMA STANDARD; PRT; 13 AA.
 ID NEUT_BUPMA
 AC P81796;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin (NT).
 OS Bufo marinus (Giant toad) (Cane toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Bufonidae; Bufo.
 OX NCBI_TaxID=8386;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Small intestine;
 RX MEDLINE=99000115; PubMed=9786176;
 RA Warner F.J., Butcher E., Carriaway R., Conlon J.M.;
 RT "Purification, characterization, and spasmogenic activity of
 neurotensin from the toad Bufo marinus.";
 RL Peptides 19:1255-1261(1998).
 CC -1- FUNCTION: Smooth muscle-contracting peptide. Peptide action is not
 affected by tetrodotoxin, but is slightly mediated through the
 release of acetylcholine.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the neurotensin family.
 KW Vasoactive; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 1 1
 SQ SEQUENCE 13 AA; 1515 MW; 56BD9F3A5410DD3 CRC64;
 QY Query Match 25.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 7 PYTL 10
 10 PYTL 13

RESULT 6

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NEUT_CAVPO
ID NEUT_CAVPO STANDARD; PRT; 13 AA.
AC P32560;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin (NT).
GN NTS.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=86248085; PubMed=3087775;
RA Shaw C., Thim L., Conlon J.M.;
RT "Ser7/neurotensin: isolation from guinea pig intestine.";
RL FEBS Lett. 202:187-192(1986).
CC -1- FUNCTION: Smooth muscle-contracting peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the neurotensin family.
DR PIR; A53608; A53608.
KW Vasocactive; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
DB 10 PYTL 13

RESULT 7
NEUT_CHICK
ID NEUT_CHICK STANDARD; PRT; 13 AA.
AC P13724;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin (NT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=88063566; PubMed=3682409;
RA Iwabuchi H., Komori S., Ohashi H., Kilmura S.;
RT "The amino acid sequence of a smooth muscle-contracting peptide from
RT chicken rectum. Identity to chicken neurotensin.";
RL Jpn. J. Pharmacol. 44:455-459(1987).
CC -1- FUNCTION: Smooth muscle-contracting peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the neurotensin family.
DR PIR; A28505; A28505.
KW Vasocactive; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 13 AA; 1608 MW; 4C949E714C410D3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
DB 10 PYTL 13

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RESULT 8
NEUT_RANTE
ID NEUT_RANTE STANDARD; PRT; 13 AA.
AC P41536;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin (NT).
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RX MEDLINE=92245104; PubMed=1574601;
RA Shaw C., McKay D.M., Halton D.W., Thim L., Buchanan K.D.;
RT "Isolation and primary structure of an amphibian neurotensin.";
RL Regul. Pept. 38:23-31(1992).
CC -1- FUNCTION: Smooth muscle-contracting peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Identified in brain, intestine, and rectum,
CC but not in stomach or skin.
CC -1- SIMILARITY: Belongs to the neurotensin family.
DR PIR; A61067; A61067.
KW Vasocactive; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 13 AA; 1569 MW; 56A53D69EF410D3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
DB 10 PYTL 13

RESULT 9
TY13_PHYRO
ID TY13_PHYRO STANDARD; PRT; 13 AA.
AC P04056;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gorzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 QVSPY 8
DB 1 QEKPY 5

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RESULT 10

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PEDI_HYDAT
ID PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Pedin. 1996 (Rel. 34, Last annotation update)
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Hydrozoa; Hydroids; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxId=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=66232307; PubMed=6674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RL peptides from Hydra vulgaris."
RL Development 122:1941-1948(1996).
CC -1- FUNCTION: Morphogenetically active peptide. Active in foot
development.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 23.9%; Score 16; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQVSPYTL 10
DB 1 EELRPEVL 8

RESULT 11
PROX ORYSA STANDARD; PRT; 13 AA.
ID PROX ORYSA STANDARD; PRT; 13 AA.
AC P83647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable profilin LP04 (Fragments).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Indica-IR64; TISSUE=Panicle;
RA Hosseini Salekdeh S.G.; Bennett J.;
RT "Proteome analysis of rice panicle."
RL Submitted (JUL-2003) to Swiss-Prot.
CC -1- FUNCTION: Binds to actin and affects the structure of the
cytoskeleton. At high concentrations, profilin prevents the
polymerization of actin, whereas it enhances it at low
concentrations. By binding to PIP2, it inhibits the formation of
IIB and DG (by similarity).
CC -1- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
actin in a 1:1 ratio.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 4.4, its MW is: 14.0 kDa.
CC -1- SIMILARITY: Belongs to the profilin family.
DR PROSITE; PS00414; PROFILIN; PARTIAL.
KM Actin-binding; Cytoskeleton; Multigene family.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 5
FT NON_TER 6
SQ SEQUENCE 13 AA; 1362 MW; OA3022E0E52C66B CRC64;

Query Match 23.9%; Score 16; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 5e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 YTLKLG 13

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DB 6 YWVIQG 11

RESULT 12
SA2A_ONCMY STANDARD; PRT; 13 AA.
ID SA2A_ONCMY STANDARD; PRT; 13 AA.
AC P82238;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Salmocidin 2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxId=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Sera;
RA Henry M.A.; Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RL from rainbow trout, Oncorhynchus mykiss."
RL Submitted (DEC-1999) to Swiss-Prot.
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AF6C45873 CRC64;

Query Match 23.9%; Score 16; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 LKLG 13
DB 4 VLKG 7

RESULT 13
SA2B_ONCMY STANDARD; PRT; 13 AA.
ID SA2B_ONCMY STANDARD; PRT; 13 AA.
AC P82239;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 42, Last annotation update)
DE Salmocidin 2B (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxId=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Sera;
RA Henry M.A.; Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RL from rainbow trout, Oncorhynchus mykiss."
RL Submitted (DEC-1999) to Swiss-Prot.
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1400 MW; 5FFB792AEAB5873 CRC64;

Query Match 23.9%; Score 16; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 LKLG 13

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Db          4 VLKG 7

RESULT 14
ACT7_SOYBN  STANDARD; PRT; 13 AA.
ID ACT7_SOYBN  STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SACT7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes."
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells.
CC -!- FUNCTION: Essential component of cell cytoskeleton; plays an
CC important role in cytoplasmic streaming, cell shape determination,
CC cell division, organelle movement and extension growth.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X17120; CAA34980.1; -.
DR PIR, S15755; S15755.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON TER 13
FT SEQUENCE 13 AA; 1420 MM; 8BEFF3C36D4FD05A CRC64;
SQ
Query Match 22.4%; Score 15; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQVSP 7
| : |
| : |
Db 5 EDIOP 9

RESULT 15
E121_LITRU  STANDARD; PRT; 13 AA.
ID E121_LITRU  STANDARD; PRT; 13 AA.
AC P83097;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litorea rubella (Desert tree frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litorea.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Mabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litorea electrica. Comparison with the skin peptides from Litorea
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13
FT SEQUENCE 13 AA; 1599 MM; C1808EF326F57322 CRC64;
SQ
Query Match 22.4%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOBO 4
| : |
| : |
Db 1 NEEB 4

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Search completed: October 1, 2004, 13:48:13
Job time : 11 secs

Blank Sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 13:46:59 ; Search time 37 Seconds

(without alignments)
110.858 Million cell updates/sec

Title: US-09-674-616A-2
Perfect score: 67
Sequence: 1 NQEQVSPYTLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 436

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	32.8	13	4 Q9UEE2	Q9uee2 homo sapien
2	19	28.4	13	2 O51605	O51605 escherichia
3	19	28.4	13	2 O9RG00	O9rg00 mycoplasma
4	19	28.4	13	4 O14890	O14890 homo sapien
5	18	26.9	13	2 O48357	O48357 escherichia
6	17	25.4	13	2 O50476	O50476 mycobacteri
7	16	23.9	13	3 O93824	O93824 candida tro
8	16	23.9	13	10 O9FSA8	O9fsa8 silene bacc
9	16	23.9	13	10 O9FS8N1	O9fsn1 hordeum vul
10	16	23.9	13	10 O9FS94	O9fs94 silene pent
11	15	22.4	13	2 O47693	O47693 escherichia
12	15	22.4	13	2 O9RFZ4	O9rfz4 mycoplasma
13	15	22.4	13	11 O9QW45	O9qw45 rattus sp.
14	15	22.4	13	11 O9QY46	O9qy46 mus sp. zfp
15	15	22.4	13	11 O88176	O88176 mus muscula
16	14	20.9	13	2 Q9R8R9	Q9r8r9 streptococc

17	14	20.9	13	2 O31295	O31295 buchnera ap
18	14	20.9	13	4 Q96Q66	Q96q66 homo sapien
19	14	20.9	13	4 Q86V06	Q86v06 homo sapien
20	14	20.9	13	5 O61340	O61340 panulirus i
21	14	20.9	13	8 Q8WEJ9	Q8wej9 ginkgo bilo
22	14	20.9	13	10 P82432	P82432 nicotiana t
23	14	20.9	13	11 Q8CJ33	Q8cj33 mus muscula
24	14	20.9	13	11 Q80Y03	Q80y03 rattus sp.
25	14	20.9	13	13 P82848	P82848 rana pipien
26	13	19.4	13	3 P87031	P87031 saccharomyc
27	13	19.4	13	4 Q9UEE3	Q9uee3 homo sapien
28	13	19.4	13	4 Q14461	Q14461 homo sapien
29	13	19.4	13	5 P83567	P83567 sepi offic
30	13	19.4	13	8 Q8WGC2	Q8wgc2 isochloes p
31	13	19.4	13	8 Q85LH3	Q85lh3 plectura m
32	13	19.4	13	12 Q9E1V2	Q9e1v2 hepatitis b
33	13	19.4	13	12 Q9E1U6	Q9e1u6 hepatitis b
34	13	19.4	13	12 Q9E1U5	Q9e1u5 hepatitis b
35	13	19.4	13	12 Q9E1U0	Q9e1u0 hepatitis b
36	13	19.4	13	12 Q9E1T9	Q9e1t9 hepatitis b
37	13	19.4	13	12 Q9E1T8	Q9e1t8 hepatitis b
38	13	19.4	13	12 Q9E1U4	Q9e1u4 hepatitis b
39	13	19.4	13	12 Q9E1U9	Q9e1u9 hepatitis b
40	13	19.4	13	12 Q9WMS5	Q9wms5 sigma virus
41	13	19.4	13	12 Q9E1V4	Q9e1v4 hepatitis b
42	13	19.4	13	12 Q9E1V4	Q9e1v4 hepatitis b
43	13	19.4	13	12 Q9E1U2	Q9e1u2 hepatitis b
44	13	19.4	13	12 Q86129	Q86129 vesicular s
45	13	19.4	13	12 Q86129	Q86129 vesicular s

ALIGNMENTS

RESULT 1

Q9UEE2 PRELIMINARY; PRT; 13 AA.
ID Q9UEE2
AC Q9UEE2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ERGB transcription factor (fragment).
GN FLIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
RT "Molecular analysis on the breakpoint region of a t(11:22)
RL translocation in Ewing's sarcoma.";
DR EMBL, AB012625; BAA32806.1; .
FT NON_TER
FT NON_TER
SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 32.8%; Score 22; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 QVSPYTL 11
DB 5 QPDYQIL 12

RESULT 2
ID O51605 PRELIMINARY; PRT; 13 AA.
AC O51605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE CE1E7 protein (Fragment).
GN CE1E7.
OS Escherichia coli.
OC Plasmid COLB7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92293113; PubMed=1603061;
RA Soong B.W., Lu F.M., Chak K.F.;
RT "Characterization of the cea gene of the COLB7 plasmid.";
DR MOL. Gen. Genet. 233:177-183(1992).
DE EMBL; M62409; AAA9805.1; -.
GO; GO:0046821; C:extrachromosomal DNA, IEA.
DR InterPro; IPR000290; Colicin_pycocin.
DR Pfam; PF01320; Colicin_Pycocin; 1.
KM plasmid.
FT NON_TER
SQ SEQUENCE 13 AA; 1501 MW; 9E75F892148CB045 CRC64;

Query Match 28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 QEOVSPPT 9
ID Q9RG00 PRELIMINARY; PRT; 13 AA.
AC Q9RG00;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Hypothetical protein (Fragment).
OS Mycoplasma capricolum subsp. capricolum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=40479;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=8035;
RA MEDLINE=20193983; PubMed=10727835;
RA Thiaucourt F., Lorenzon S., David A., Breard A.;
RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT of a putative membrane protein gene.";
RL Vet. Microbiol. 72:251-268(2000).
DR EMBL; AF162995; AAF15247.1; -.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 13 AA; 1459 MW; 0B63638AED35573B CRC64;

Query Match 28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 SPYTLK 12
ID Q14890 PRELIMINARY; PRT; 13 AA.
AC Q14890;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Mucin (Fragment).
GN MUC5AC.
RN (1)

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```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX TISSUE=Tracheobronchial mucosa;
RA Guyonnet-Duperrat V., Audie J., Debailleul V., Laine A., Bulsine M.,
RA Zoultina-Gallieue S., Pigny P., Degand P., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus
RT cysteine-rich domain for 11p15 mucin genes.";
RL Biochem. J. 0:0-0(1994).
DR EMBL; Z34280; CAA84034.1; -.
FT NON_TER
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match 28.4%; Score 19; DB 4; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQROVSP 7
ID Q48357 PRELIMINARY; PRT; 13 AA.
AC Q48357;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Transcription termination factor rho (Fragment).
GN RHO.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95129907; PubMed=7828920;
RA Opperman T., Martinez A., Richardson J.P.;
RT "The ts15 mutation of Escherichia coli alters the sequence of the C-
RT terminal nine residues of Rho protein.";
RL Gene 152:133-134(1995).
DR EMBL; L34404; AAA68985.1; -.
FT NON_TER
SQ SEQUENCE 13 AA; 1531 MW; 93F7EB96FDBECB1A CRC64;

Query Match 26.9%; Score 18; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQEQVSP 7
ID Q50476 PRELIMINARY; PRT; 13 AA.
AC Q50476;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Catalase.
GN KATG.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN (1)

```

```

RESULT 6
QY 50476
ID Q50476 PRELIMINARY; PRT; 13 AA.
AC Q50476;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Catalase.
GN KATG.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN (1)

```

RP SEQUENCE FROM N.A.
 RC STRAIN=110373;
 RA Cockerill F.R., Uh1 J.R., Temessen Z., Zhang Y., Stockman L.,
 RA Roberts G.D., Williams D.L., Kline B.C.;
 RT "Rapid identification of a point mutation of the *Mycobacterium*
 RT *tuberculosis* catalase-peroxidase (katG) gene associated with isoniazid
 RT resistance".
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U06263; AAB59976.1; -.
 SQ SEQUENCE 13 AA; 1564 MW; 2F39A45EFE994777 CRC64;

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 2.7e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EOVSPYT 9
 DB 3 EQHPPT 9

RESULT 7
 ID 093824 PRELIMINARY; PRT; 13 AA.
 AC 093824;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, last sequence update)
 DT 01-MAY-1999 (TEMBLrel. 10, last annotation update)
 DE UDP-galactose-4-epimerase (Fragment).
 GN GAL10.
 OS *Candida tropicalis* (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5482;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PK233;
 RA Kanai T., Ueda M., Tanaka A.;
 RT "Candida tropicalis promoter region of GAL1 and GAL10 gene."
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB019434; BAA34351.1; -.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1312 MW; 0B559D6AE18BC720 CRC64;

Query Match 23.9%; Score 16; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.2e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YTLKG 13
 DB 5 YILVTG 10

RESULT 8
 ID 09FS48 PRELIMINARY; PRT; 13 AA.
 AC 09FS48;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS *Silene bacillifera* (Berry catchfly) (Cucubalus bacillifer).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=54818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid *Silene aegaea*
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data."
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ296139; CAC13015.1; -.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;

Query Match 23.9%; Score 16; DB 10; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.2e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPYT 9
 DB 1 TPPT 4

RESULT 9
 ID 09S8N1 PRELIMINARY; PRT; 13 AA.
 AC 09S8N1;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, last annotation update)
 DE Calmodulin (Fragment).
 OS *Hordeum vulgare* (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94266769; PubMed=8206888;
 RA Toda H., Yazawa M., Sakiyama F., Yeji K.;
 RT "Amino acid sequence of calmodulin from wheat germ."
 RT J. Biochem. 115:367-367(1994).
 SQ SEQUENCE 13 AA; 1508 MW; 9763F31CD43DB1A CRC64;

Query Match 23.9%; Score 16; DB 10; Length 13;
 Best Local Similarity 33.3%; Pred. No. 4.2e+04;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EOVSPY 8
 DB 7 EQTAEP 12

RESULT 10
 ID 09FS94 PRELIMINARY; PRT; 13 AA.
 AC 09FS94;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, last annotation update)
 DE RNA polymerase II (Fragment).
 GN RPB2.
 OS *Silene pentelica*.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=49735;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Popp M., Oxelman B.;
 RT "Inferring the history of the polyploid *Silene aegaea*
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data."
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296132; CAC13024.1; -.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;

Query Match 23.9%; Score 16; DB 10; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.2e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPYT 9
: :
DB 1 TFFT 4

RESULT 11
ID Q47693 PRELIMINARY; PRT; 13 AA.
AC Q47693;

DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Elongation factor TU (EF-TU) (Fragment).
GN TUBB.
OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;

RP SEQUENCE FROM N.A.
RX MEDLINE=82080657; PubMed=7312036;

RA Hudson L., Rossi J., Landy A.;
RL Nature 294:422-427(1981).
RT "Dual function transcripts specifying tRNA and mRNA.";

DR EMBL; X04181; CAA27777.1; -;
DR GO; GO:0003746; P:translation elongation factor activity; IEA.
KW Elongation factor; Protein biosynthesis.

FT NON TER 13
SQ SEQUENCE 13 AA; 1617 MW; C433BE82A18D0B19 CRC64;

Query Match 22.4%; Score 15; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EQVSPY 8
: :
DB 7 ERTKPH 12

RESULT 12
ID Q9RFZ4 PRELIMINARY; PRT; 13 AA.
AC Q9RFZ4;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).
OS Mycoplasma mycoides subsp. capri.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

NCBI_TaxID=40477;
RP SEQUENCE FROM N.A.
RX STRAIN=EG3;

RA MEDLINE=20193983; PubMed=10727835;
RA Thaucourt F., Lorenzon S., David A., Breard A.;
RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT Vet. Microbiol. 72:251-268(2000).
RL Vet. Microbiol. 72:251-268(2000).

DR EMBL; AF162998; AAF15253.1; -;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 13 AA; 1505 MW; 0B79431F5635573B CRC64;

Query Match 22.4%; Score 15; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.5e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PYTL 10
: :
DB 5 PYLI 8

RESULT 13
ID Q9QW45 PRELIMINARY; PRT; 13 AA.
AC Q9QW45;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE GTP-binding protein RAB16 (Fragment).

OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.

RX MEDLINE=93054572; PubMed=1429617;
RA Elferink L.A., Anzai K., Scheller R.H.;
RT "Rab15, a novel low molecular weight GTP-binding protein specifically
RT expressed in rat brain";
RL J. Biol. Chem. 267:22693-22693(1992).

FT NON TER 1
SQ SEQUENCE 13 AA; 1584 MW; 40BD5FE7236041A3 CRC64;

Query Match 22.4%; Score 15; DB 11; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QVSPYT 9
: :
DB 4 QIKTYS 9

RESULT 14
ID Q9QY46 PRELIMINARY; PRT; 13 AA.
AC Q9QY46;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE Zfp127 protein (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10095;
RP SEQUENCE FROM N.A.

RX MEDLINE=20056261; PubMed=10588722;
RA Greally J.M., Gray T.A., Gabriel J.M., Song L., Zemel S.,
RA Nicholas R.D.;
RT "Conserved characteristics of heterochromatin-forming DNA at the
RT 15q11-q13 imprinting center.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:14430-14435(1999).
DR EMBL; AF130348; AAD56756.1; -;
FT NON TER 13
SQ SEQUENCE 13 AA; 1356 MW; D89F5BA9529476D CRC64;

Query Match 22.4%; Score 15; DB 11; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QEOVSP 7
: :
DB 2 EESTAP 7

RESULT 15
ID Q88176 PRELIMINARY; PRT; 13 AA.
AC Q88176;

DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).

GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb-c; TISSUE=Liver;
 RX MEDLINE=98250618; PubMed=9582442;
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
 RT "A cis-acting regulatory element that affects the alternative splicing
 of a muscle-specific exon in the mouse NCAM gene.";
 RL Biochim. Biophys. Acta 1397:305-315(1998).
 DR EMBL; AB001673; BAA31275.1; -.
 DR MGD; MGI:97281; Ncam1.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1496 MW; CC6098F54C72D732 CRC64;

Query Match 22.4%; Score 15; DB 11; Length 13;
 Best Local Similarity 42.9%; Pred. No. 6.5e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 VSEPTLL 11
 : | | |
 Db 7 LQPTCT 13

Search completed: October 1, 2004, 13:50:08
 Job time : 39 secs

Blank Sheet

Fri Oct 1 13:54:09 2004

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 13:48:03 ; Search time 17 Seconds

(without alignments)
39,479 Million cell updates/sec

Title: US-09-674-616A-2

Sequence: 1 NOEQVSPYTLKG 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 6327

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCUTS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	53.7	13	4	US-09-675-922-1
2	24	35.8	13	1	US-08-174-467-6
3	24	35.8	13	3	US-08-452-071-6
4	23	34.3	13	1	US-08-620-213-3
5	23	34.3	13	2	US-08-542-686-1
6	23	34.3	13	2	US-08-332-562A-69
7	22	33.8	13	1	US-08-068-947-14
8	22	33.8	13	1	US-08-068-947-15
9	22	33.8	13	3	US-08-068-947-22
10	22	32.8	13	4	US-09-468-578-11
11	22	32.8	13	4	US-09-868-839-11
12	22	32.8	13	4	US-09-811-672-19
13	21	31.3	13	4	US-08-068-947-19
14	20.5	30.6	13	3	US-09-040-216-8
15	20	29.9	13	1	US-08-068-947-21
16	20	29.9	13	3	US-08-630-916A-6
17	20	29.9	13	3	US-08-630-916A-6
18	20	29.9	13	4	US-08-630-916A-6
19	20	29.9	13	4	US-09-297-369A-7
20	20	29.9	13	4	US-09-635-872A-52
21	20	29.9	13	4	US-09-636-077A-52
22	20	29.9	13	4	US-09-543-608A-29
23	20	29.9	13	4	US-09-543-608A-30
24	20	29.9	13	4	US-09-543-608A-31
25	20	29.9	13	4	US-09-636-060C-52
26	20	29.9	13	4	US-09-986-552-52
27	19	28.4	13	1	US-08-068-947-8

28	19	28.4	13	1	US-08-068-947-24	Sequence 24, Appl
29	19	28.4	13	1	US-08-469-005A-13	Sequence 13, Appl
30	19	28.4	13	1	US-08-188-426-7	Sequence 7, Appl
31	19	28.4	13	1	US-08-471-033-11	Sequence 11, Appl
32	19	28.4	13	2	US-08-471-044-11	Sequence 11, Appl
33	19	28.4	13	2	US-08-463-483A-11	Sequence 11, Appl
34	19	28.4	13	2	US-08-469-009-7	Sequence 7, Appl
35	19	28.4	13	2	US-08-471-046A-11	Sequence 11, Appl
36	19	28.4	13	2	US-08-470-566B-11	Sequence 11, Appl
37	19	28.4	13	2	US-08-469-007-7	Sequence 7, Appl
38	19	28.4	13	2	US-08-838-219B-11	Sequence 11, Appl
39	19	28.4	13	2	US-08-469-334-11	Sequence 11, Appl
40	19	28.4	13	3	US-08-630-916A-58	Sequence 58, Appl
41	19	28.4	13	3	US-08-881-094-42	Sequence 42, Appl
42	19	28.4	13	3	US-09-300-529-11	Sequence 11, Appl
43	19	28.4	13	3	US-09-233-336A-11	Sequence 11, Appl
44	19	28.4	13	3	US-09-233-752A-11	Sequence 11, Appl
45	19	28.4	13	3	US-09-094-557-5	Sequence 5, Appl

ALIGNMENTS

```

RESULT 1
US-09-675-922-1
; Sequence 1, Application US/09675922
; Patent No. 6468731
; GENERAL INFORMATION:
; APPLICANT: Hubbell A., Jeffrey
; APPLICANT: Schenck C., Jason
; APPLICANT: Sakiyama E., Shelley
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
; FILE REFERENCE: ETH 107 DIV
; CURRENT APPLICATION NUMBER: US/09/675,922
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Factor XIIIa at
; OTHER INFORMATION: N-terminus and modified peptide from the
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: dansyl leucine
US-09-675-922-1

Query Match
Best Local Similarity 53.7%; Score 36; DB 4; Length 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOEQVSP 7
|||
Db 2 NOEQVSP 8

RESULT 2
US-08-174-467-6
; Sequence 6, Application US/08174467
; Patent No. 5451514
; GENERAL INFORMATION:
; APPLICANT: BOUDET, ALAIN M.
; APPLICANT: INZE, DIRK G.
; APPLICANT: SCHUCH, WOLFGANG W.
; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: CUSHMAN, DARBY & CUSHMAN

```

STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,467
FILING DATE: 28-DEC-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 95563/PS36321/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-174-467-6

Query Match 35.8%; Score 24; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VSPYT 9
Db 5 LSPYT 9

RESULT 3
US-08-452-071-6
Sequence 6, Application US/08452071
Patent No. 6066780
GENERAL INFORMATION:
APPLICANT: BOUBET, ALAIN M.
APPLICANT: INZE, DIRK G.
APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,071
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 95563/PS36321/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-452-071-6

Query Match 35.8%; Score 24; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VSPYT 9
Db 5 LSPYT 9

RESULT 4
US-08-620-213-3
Sequence 3, Application US/08620213
Patent No. 5677297
GENERAL INFORMATION:
APPLICANT: WALDECK, Harald
APPLICANT: HOELTJE, Dagmar
APPLICANT: MESSINGER, Josef
APPLICANT: ANTEL, Jochem
APPLICANT: WURL, Michael
APPLICANT: THORMAEHLER, Dirk
TITLE OF INVENTION: BENZAZEPINE-, BENZOAZEPINE- AND
TITLE OF INVENTION: BENZOTHAZEPINE-N-ACETIC ACID DERIVATIVES. PROCESS FOR THEIR
TITLE OF INVENTION: PREPARATION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,213
FILING DATE:
CLASSIFICATION: 544
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 10 566.4
FILING DATE: 23-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 181/42626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-213-3

Query Match 34.3%; Score 23; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 EQVSPYTLK 10
Db 5 EHVPYGL 12

RESULT 5

US-08-542-686-1
; Sequence 1, Application US/08542686
; Patent No. 5824487
; GENERAL INFORMATION:
; APPLICANT: Ravetch, Jeffrey V.
; APPLICANT: Kurosaki, Tomohiro
; TITLE OF INVENTION: METHOD FOR SCREENING FOR TARGETS FOR
; TITLE OF INVENTION: ANTI-INFLAMMATORY OR ANTI-ALLERGIC AGENTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,686
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,269
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John J.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42113/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-542-686-1

Query Match 34.3%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQVSPYTLK 12
Db 2 ENTITSLK 11

RESULT 6
US-08-332-562A-69
; Sequence 69, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.

APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,457
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-562A-69

Query Match 34.3%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 EQVSPYTLK 12
Db 1 ENTITSLK 10

RESULT 7
US-08-068-947-14
; Sequence 14, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepelev, Nikolai
; APPLICANT: Isakov, Olga
; APPLICANT: Krichak, Viktor
; APPLICANT: Lebl, Michel
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,947
FILING DATE: 19930528
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock Esq., S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7156-040-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-068-947-14

Query Match 32.8%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.7e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NQGVSP 7
|:|:|
Db 1 NADQIQ 7

RESULT 8

US-08-068-947-15
Sequence 15, Application US/08068947
Patent No. 5470753
GENERAL INFORMATION:
APPLICANT: Sepetov, Nikolai
APPLICANT: Lesakova, Olga
APPLICANT: Krchnak, Viktor
APPLICANT: Ieb1, Michal
TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
NUMBER OF SEQUENCES: 47
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,947
FILING DATE: 19930528
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock Esq., S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7156-040-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-068-947-15

Query Match 32.8%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGVSP 7
|:|:|
Db 2 QDQIQ 7

RESULT 9

US-08-750-419A-22
Sequence 22, Application US/08750419A
Patent No. 6008340
GENERAL INFORMATION:
APPLICANT: BALL, TANJA
APPLICANT: VITALA, SUSANNE
APPLICANT: SPERR, WOLFGANG
APPLICANT: VALENT, PETER
APPLICANT: SUSANI, MARKUS
APPLICANT: KRAFT, DIETRICH
APPLICANT: LAFFER, SYLVIA
TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, VECTORS AND HOSTS
TITLE OF INVENTION: CORRESPONDING RECOMBINANT DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES OF SAID ALLERGENS AND FRAGMENTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,419A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1614-175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-750-419A-22

Query Match 32.8%; Score 22; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QGVSPY 8
|:|:|
Db 1 EPIADY 6

RESULT 10
US-09-468-578-11

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; Sequence 11, Application US/09468578
; Patent No. 639329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-468-578-11
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Query Match          32.8%; Score 22; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 4 QVSPY 8
Db 3 QVMPY 7
```

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RESULT 11
US-09-868-839-11
; Sequence 11, Application US/09868839
; Patent No. 6509307
; GENERAL INFORMATION:
; APPLICANT: UNILEVER N.V. et al.
; TITLE OF INVENTION: DETERGENT COMPOSITIONS COMPRISING PHENOL OXIDIZING
; FILE REFERENCE: C7516(V)
; CURRENT APPLICATION NUMBER: US/09/868,839
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-868-839-11
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```
Query Match          32.8%; Score 22; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 4 QVSPY 8
Db 3 QVMPY 7
```

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RESULT 12
US-09-811-672-19
; Sequence 19, Application US/09811672
; Patent No. 6553120
; GENERAL INFORMATION:
; APPLICANT: BALI, Tanja
; APPLICANT: VITALA, Susanne
; APPLICANT: SPERR, Wolfgang
; APPLICANT: VALENT, Peter
; APPLICANT: SUSANI, Markus
; APPLICANT: KRAFT, Dietrich
```

```
; APPLICANT: VALENTA, Rudolf
; APPLICANT: LAFFER, Sylvia
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT
; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGNOSTIC
; FILE REFERENCE: 1614-0247P
; CURRENT APPLICATION NUMBER: US/09/811,672
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Timothy Grass
US-09-811-672-19
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```
Query Match          32.8%; Score 22; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 EQVSPY 8
Db 1 EPIAPY 6
```

```
RESULT 13
US-08-068-947-19
; Sequence 19, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepelov, Nikolai
; APPLICANT: Issakova, Olga
; APPLICANT: Kirchak, Viktor
; APPLICANT: Leb1, Michael
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,947
; FILING DATE: 19930528
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock Esq., S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-040-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-068-947-19
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```
Query Match          31.3%; Score 21; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 NOQVSP 7
| : | : |
Db 1 NEGQIQP 7

RESULT 14

US-09-040-216-8
; Sequence 8, Application US/09040216
; Patent No. 6030942
; GENERAL INFORMATION:
; APPLICANT: COOPERMAN, ET AL., BARRY
; TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
; TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF
; TITLE OF INVENTION: RIBONUCLEOTIDE REDUCTASE
; FILE REFERENCE: 9596-63U1
; CURRENT APPLICATION NUMBER: US/09/040,216
; CURRENT FILING DATE: 1998-03-17
; EARLIER APPLICATION NUMBER: 08/919,748
; EARLIER FILING DATE: 1997-08-28
; EARLIER APPLICATION NUMBER: 60/025,146
; EARLIER FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: alpha 13 helix region of E. coli R1
US-09-040-216-8

Query Match 30.6%; Score 20.5; DB 3; Length 13;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 8 YT-LKKG 13
| : | : | : |
Db 5 YTRLKKG 11

RESULT 15

US-08-068-947-21
; Sequence 21, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Segetov, Nikolai
; APPLICANT: Issakova, Olga
; APPLICANT: Kirchnak, Viktor
; APPLICANT: Lebl, Michal
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,947
; FILING DATE: 19930528
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock Esq., S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-040-999

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-068-947-21

Query Match 29.9%; Score 20; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVSPY 8
| : | : | : |
Db 9 QVTFP 13

Search completed: October 1, 2004, 13:50:30
Job time : 18 secs


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RESULT 2
US-09-932-613-156
; Sequence 156, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belter, James P.
; APPLICANT: Poter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-156
Query Match      35.8%; Score 24; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 QVSPYTLK 12
      |||||
      2 QVDEPTGLK 10

Db

RESULT 3
US-09-932-322-156
; Sequence 156, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Belter, James P.
; APPLICANT: Poter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Laderer, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-156
Query Match      35.8%; Score 24; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 QVSPYTLK 12
      |||||
      2 QVDEPTGLK 10

Db

RESULT 4
US-10-361-208-64
; Sequence 64, Application US/10361208
; Publication No. US20040009167A1
; GENERAL INFORMATION:
; APPLICANT: Rider, Todd H.
; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
```

```
; FILE REFERENCE: 0050.2041-003
; CURRENT APPLICATION NUMBER: US/10/361,208
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,359
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,022
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/432,386
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: partial Hdj-1 sequence
; NAME/KEY: NON_CONS
; LOCATION: 7-8
US-10-361-208-64
Query Match      35.8%; Score 24; DB 15; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QEOVSP 7
      |||||
      7 QEOVLP 12

Db

RESULT 5
US-10-361-208-197
; Sequence 197, Application US/10361208
; Publication No. US20040009167A1
; GENERAL INFORMATION:
; APPLICANT: Rider, Todd H.
; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
; FILE REFERENCE: 0050.2041-003
; CURRENT APPLICATION NUMBER: US/10/361,208
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,359
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,022
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/432,386
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 13
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: partial Hdj-1 sequence
; NAME/KEY: NON_CONS
; LOCATION: 7-8
US-10-361-208-197
Query Match      35.8%; Score 24; DB 15; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 QEOVSP 7
      |||||
      7 QEOVLP 12

Db

RESULT 6
US-10-226-007-782
; Sequence 782, Application US/10226007
; Publication No. US20030105277A1
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```
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 782
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-782
```

```
Query Match          34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 NOEQVSPY 8
Db      1 NEEPPPPY 8
```

```
RESULT 7
US-10-226-007-794
; Sequence 794, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-794
```

```
Query Match          34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 NOEQVSPY 8
Db      2 NEEPPPPY 9
```

```
RESULT 8
US-10-226-007-805
; Sequence 805, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
```

```
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 805
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-805
```

```
Query Match          34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 NOEQVSPY 8
Db      3 NEEPPPPY 10
```

```
RESULT 9
US-10-226-007-815
; Sequence 815, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 815
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-815
```

```
Query Match          34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 NOEQVSPY 8
Db      4 NEEPPPPY 11
```

```
RESULT 10
US-10-226-007-824
; Sequence 824, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 824
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-824
```

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NOEQVSPY 8
|:|:|
Db 5 NEEPPPPY 12

RESULT 11

US-10-226-007-832
; Sequence 832, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavit, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 832
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-832

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NOEQVSPY 8
|:|:|
Db 6 NEEPPPPY 13

RESULT 12

US-10-412-897-20
; Sequence 20, Application US/10412897
; Publication No. US2003022022A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYPEPTIDES ENCODING THE HUMAN CITRON KINASE
; FILE REFERENCE: D0193 NP
; CURRENT APPLICATION NUMBER: US/10/412,897
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: U.S. 60/372,745
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-897-20

Query Match 34.3%; Score 23; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 OEQVS 6
|:|:|
Db 2 OEQVS 6

RESULT 13

US-09-338-723A-7

; Sequence 7, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachyotrys chartarum
US-09-338-723A-7

Query Match 32.8%; Score 22; DB 9; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVSPY 8
|:|:|
Db 3 QVMPY 7

RESULT 14

US-09-811-672-19
; Sequence 19, Application US/09811672
; Patent No. US20020052490A1
; GENERAL INFORMATION:
; APPLICANT: BALL, Tanja
; APPLICANT: VITALA, Susanne
; APPLICANT: SPER, Wolfgang
; APPLICANT: VALENT, Peter
; APPLICANT: SUSANI, Markus
; APPLICANT: KRAFT, Dietrich
; APPLICANT: VALENTA, Rudolf
; APPLICANT: LAFFER, Sylvia
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT
; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGN
; FILE REFERENCE: 1614-0247P
; CURRENT APPLICATION NUMBER: US/09/811,672
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Timothy Grass
US-09-811-672-19

Query Match 32.8%; Score 22; DB 9; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EQVSPY 8
|:|:|
Db 1 EPIARY 6

RESULT 15

US-09-946-175-8
; Sequence 8, Application US/09946175
; Patent No. US20020106671A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: IDENTIFICATION OF A CAPACITATIVE CALCIUM
; FILE REFERENCE: CHANNEL IN ANTIGEN PRESENTING CELLS AND USES THEREOF
US-09-946-175-8

```

; CURRENT APPLICATION NUMBER: US/09/946,175
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-946-175-8

```

```

Query Match          32.8%; Score 22; DB 9; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.2e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 5 VSPYTLKG 13
   :||::|
Db 4 LSPYVMIG 12

```

```

Search completed: October 1, 2004, 13:49:24
Job time : 46 secs

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Blank Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 13:46:58 ; Search time 51 Seconds
(without alignments)

72.022 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67
Sequence: 1 NQEOVSPYTLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 15593

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	100.0	13	3	AAV67835 Alpha-2 a
2	64	95.5	13	3	AAV67837 Alpha-2 a
3	61	91.0	13	3	AAV67836 Alpha-2 a
4	61	91.0	13	3	AAV67842 Alpha-2 a
5	59	88.1	13	3	AAV67841 Alpha-2 a
6	59	88.1	13	3	AAV67840 Alpha-2 a
7	46	68.7	13	3	AAV67844 Alpha-2 a
8	46	68.7	13	3	AAV67844 Alpha-2 a
9	36	53.7	13	6	AAV673917 Factor XI
10	27	40.3	13	2	AAV20946 Human pro
11	26	38.8	13	2	AAV20420 Human mic
12	25	37.3	13	2	AAV54972 Scythi gta
13	25	37.3	13	2	AAV38008 WW domain
14	25	37.3	13	5	AAE23145 Influenza
15	24	35.8	13	2	AAV34779 CAD trypt
16	24	35.8	13	5	ABJ00698 B lymphoc
17	24	35.8	13	5	ABG33559 B lymphoc
18	24	35.8	13	5	ABB97726 Human pro
19	24	35.8	13	5	ABB97727 Human pro
20	23	34.3	13	2	AAV49912 Glutamin
21	23	34.3	13	2	AAV49915 Glutamin
22	23	34.3	13	2	AAV49913 Glutamin
23	23	34.3	13	2	AAV60824 Anticbody
24	23	34.3	13	2	AAV60824 Anticbody
25	23	34.3	13	2	AAV60824 Anticbody

26	23	34.3	13	4	AAV53255 Human non
27	23	34.3	13	5	ABB97728 Human pro
28	23	34.3	13	6	ADA51575 Human her
29	23	34.3	13	6	ADA51545 Human her
30	23	34.3	13	6	ADA51533 Human her
31	23	34.3	13	6	ADA51556 Human her
32	23	34.3	13	6	ADA51583 Human her
33	23	34.3	13	6	ADA51566 Human her
34	22	32.8	13	2	AAV606274 ITIM moti
35	22	32.8	13	2	AAV45224 Stachybot
36	22	32.8	13	3	AAV96766 S. charita
37	22	32.8	13	3	AAV95542 Stachybot
38	22	32.8	13	4	ABV56293 Vascular
39	22	32.8	13	4	AAU28621 DPI trypt
40	22	32.8	13	4	AAU25365 Schizophr
41	22	32.8	13	4	AAU26269 Depressio
42	22	32.8	13	4	AAU15709 Schizophr
43	22	32.8	13	5	AAO18215 S charitar
44	22	32.8	13	5	AAE17225 Peptide C
45	22	32.8	13	5	AAE17220 Peptide C

ALIGNMENTS

RESULT 1
AAV67835
ID AAV67835 standard; peptide; 13 AA.

AC AAV67835;
DT 25-APR-2000 (first entry)
XX Alpha-2 antipiasmin enzyme derived peptide #2.

DE Alpha-2 antipiasmin enzyme derived peptide #2.
XX Alpha-2 antipiasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX Synthetic.

XX Key Location/Qualifiers
FH Modified-site 1 /note="Asn optionally forms a peptide bond with C-terminal Gly to form a cyclic peptide"
FT Misc-difference 5..13 /note="Optionally D form residues"
FT Modified-site 13 /note="Gly optionally forms a peptide bond with N-terminal Asn to form a cyclic peptide"

FT W09960018-A1.

XX 25-NOV-1999.

XX 14-MAY-1999; 99WO-GB001550.

XX 15-MAY-1998; 98EP-00303872.

XX (AMSH) NYCOMED AMERSHAM PLC.

XX Storey AE, Mendisabal M, Champion S, Gibson A, Guilbert B;
PI Wilson IA, Knox P;

XX WPI; 2000-126380/11.

XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
PT atherosclerosis, inflammation or cancer.

XX Example 1; Page 16; 46pp; English.

XX This sequence represents an alpha-2 antipiasmin derived peptide. Alpha-2
CC antipiasmin is a substrate for the fibrin stabilising enzyme Factor
XX XIIIa. Synthetic analogues of lysine and glutamine labelled with a


```

XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "N-terminal acetyl"
FT Misc-difference 8
FT /note= "D-form residue"
FT Misc-difference 12
FT /note= "D-form residue"
FT Modified-site 13
FT /label= bAla
XX
XX WO960018-A1.
XX
XX PD 25-NOV-1999.
XX
XX PF 14-MAY-1999; 99WO-GB001550.
XX
XX PR 15-MAY-1998; 98EP-00303872.
XX
XX (AMSH ) NYCOMED AMERSHAM PLC.
XX
XX PA Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
XX PI Wilson IA, Knox P;
XX DR WPI; 2000-126380/11.
XX
XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
XX atherosclerosis, inflammation or cancer.
XX
XX PS Example 2; Page 17; 46pp; English.
XX
XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
XX antipiasmin is a substrate for the fibrin stabilising enzyme Factor
XX XIIIa. Synthetic analogues of lysine and glutamine labelled with a
XX detectable moiety can also act as substrates for Factor XIIIa. The
XX invention relates to compounds which can be used in the diagnosis of
XX thrombosis or embolism and also for diagnosing atherosclerosis,
XX inflammation or cancer. The peptide forms part of the compound
XX
XX SQ Sequence 13 AA;
XX
XX Query Match 91.0%; Score 61; DB 3; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NOEQVSPYTLTK 12
XX |||||
XX 1 NOEQVSPYTLTK 12
XX
XX Db
XX
XX RESULT 5
XX AA67841
XX ID AA67841 standard; peptide; 13 AA.
XX
XX AC AA67841;
XX
XX DT 25-APR-2000 (first entry)
XX
XX DE Alpha-2 antiplasmin enzyme derived peptide #8.
XX
XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
XX embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl"
XX FT Modified-site 8
XX FT /note= "2-Naphthylalanine"
XX
XX WO960018-A1.
XX

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```

PD 25-NOV-1999.
XX
XX PF 14-MAY-1999; 99WO-GB001550.
XX
XX PR 15-MAY-1998; 98EP-00303872.
XX
XX (AMSH ) NYCOMED AMERSHAM PLC.
XX
XX PA Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
XX PI Wilson IA, Knox P;
XX DR WPI; 2000-126380/11.
XX
XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
XX atherosclerosis, inflammation or cancer.
XX
XX PS Example 2; Page 16; 46pp; English.
XX
XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
XX antipiasmin is a substrate for the fibrin stabilising enzyme Factor
XX XIIIa. Synthetic analogues of lysine and glutamine labelled with a
XX detectable moiety can also act as substrates for Factor XIIIa. The
XX invention relates to compounds which can be used in the diagnosis of
XX thrombosis or embolism and also for diagnosing atherosclerosis,
XX inflammation or cancer. The peptide forms part of the compound
XX
XX SQ Sequence 13 AA;
XX
XX Query Match 88.1%; Score 59; DB 3; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 0.00038;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 NOEQVSPYTLTKG 13
XX |||||
XX 1 NOEQVSPYTLTKG 13
XX
XX Db
XX
XX RESULT 6
XX AA67840
XX ID AA67840 standard; peptide; 13 AA.
XX
XX AC AA67840;
XX
XX DT 25-APR-2000 (first entry)
XX
XX DE Alpha-2 antiplasmin enzyme derived peptide #7.
XX
XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
XX embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl"
XX
XX WO960018-A1.
XX
XX PD 25-NOV-1999.
XX
XX PF 14-MAY-1999; 99WO-GB001550.
XX
XX PR 15-MAY-1998; 98EP-00303872.
XX
XX (AMSH ) NYCOMED AMERSHAM PLC.
XX
XX PA Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
XX PI Wilson IA, Knox P;
XX DR WPI; 2000-126380/11.
XX
XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
XX atherosclerosis, inflammation or cancer.
XX

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```

XX Example 2; Page 16; 46pp; English.
PS
XX
CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
CC detectable moiety can also act as substrates for Factor XIIIa. The
CC invention relates to compounds which can be used in the diagnosis of
CC thrombosis or embolism and also for diagnosing atherosclerosis,
CC inflammation or cancer. The peptide forms part of the compound
XX
SQ Sequence 13 AA;

Query Match      88.1%; Score 59; DB 3; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00038;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOEQVSPYTLKKG 13
Db 1 NOEQVSPYTLKKG 13

RESULT 7
AA67844
ID AA67844 standard; peptide; 13 AA.
XX
AC AA67844;
XX
DT 25-APR-2000 (first entry)
XX
DE Alpha-2 antiplasmin enzyme derived peptide #11.
XX
KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX
OS Synthetic.
XX
PN W09960018-A1.
XX
PD 25-NOV-1999.
XX
PF 14-MAY-1999; 99WO-GB001550.
XX
PR 15-MAY-1998; 98EP-00303872.
XX
PA (AMSH ) NYCOMED AMERSHAM PLC.
XX
PI Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
PI Wilson IA, Knox P;
XX
DR WPI; 2000-126380/11.
XX
PT Novel synthetic analogues for diagnosis of thrombosis, embolism,
PT atherosclerosis, inflammation or cancer.
XX
PS Example 2; Page 17; 46pp; English.
XX
CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
CC detectable moiety can also act as substrates for Factor XIIIa. The
CC invention relates to compounds which can be used in the diagnosis of
CC thrombosis or embolism and also for diagnosing atherosclerosis,
CC inflammation or cancer. The peptide forms part of the compound
XX
SQ Sequence 13 AA;

Query Match      68.7%; Score 46; DB 3; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 NOEQVSPYTLKKG 13
Db 1 NOEQVSPYTLKKG 13

```

```

Db 1 NOEQVSPYAAAAG 13

RESULT 8
AAM50298
ID AAM50298 standard; peptide; 13 AA.
XX
AC AAM50298;
XX
DT 04-FEB-2002 (first entry)
XX
DE Factor XIIIa substrate-polylysine peptide chimera.
XX
KW Tissue engineering; tissue repair; tissue regeneration; drug delivery;
KW Factor XIIIa; heparin.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Modified-site 1
FH /note="dansyl leucine, allows detection of peptide by
FT fluorescence"
FT Peptide 2..8
FT /note="Factor XIIIa substrate"
FT Peptide 9..13
FT /note="heparin-binding peptide"
XX
PN W0200183522-A2.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2000; 2000WO-US011947.
XX
PR 01-MAY-2000; 2000WO-US011947.
XX
PA (R1DG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
PA (HUBER/) HUBBELL J A.
XX
PI Hubbell JA, Schense JC, Sakiyama-Elbert SE;
XX
DR WPI; 2002-041479/05.
XX
PT Novel growth factor modified protein matrix useful for tissue repair,
PT regeneration and/or remodeling, and/or drug delivery.
XX
PS Example 2; Page 25; 51pp; English.
XX
CC The present sequence is that of a fluorescent synthetic peptide, which
CC has a Factor XIIIa substrate at the N-terminal end and a polylysine
CC moiety at the C-terminus. The peptide is used to produce a heparin-
CC peptide chimera by coupling to a heparin oligosaccharide, with a unique
CC aldehyde group on one end, via reductive amination. A matrix is formed in
CC which heparin is used to incorporate heparin-binding growth factors for
CC use in tissue repair, regeneration, remodeling, and/or drug delivery. The
CC invention provides biocompatible and biodegradable matrices incorporating
CC bioactive proteins such as growth factors. The matrices can be formed in
CC vitro or in vivo at the site of implantation, and provide controlled
XX
SQ Sequence 13 AA;

Query Match      53.7%; Score 36; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOEQVSP 7
Db 2 NOEQVSP 8

RESULT 9
ABG73917
ID ABG73917 standard; peptide; 13 AA.

```



```

XX AC ABG73917;
XX XX
XX DT 27-MAR-2003 (first entry)
XX DE Factor IIIa cleavage site-containing peptide #1.
XX XX Factor XIIIa; fibrin matrix; heparin; heparin binding protein; HBP;
XX KM wound healing; vasculature; skin; nerve; liver.
XX XX
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /label= OTHER
XX FT /note= "Dansyl-leucine, used to allow detection by
XX FT fluorescence"
XX FT
XX PN US6468731-B1.
XX XX
XX PD 22-OCT-2002.
XX XX
XX PF 29-SEP-2000; 2000US-00675922.
XX PR 27-AUG-1998; 98US-00141153.
XX XX
XX PA (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
XX PA (UYZU-) UNIV ZUERICH.
XX PI Hubbell JA, Schense JC, Sakiyama SE;
XX XX
XX DR WPI; 2003-155552/15.
XX XX
XX PT Novel matrix for controlled delivery of heparin binding protein has
XX PT fibrin, peptide having first domain with Factor XIIIa substrate and
XX PT second domain with heparin/heparin-like compound, and heparin binding
XX PT protein.
XX XX
XX PS Example 2; Col 6; 17pp; English.
XX XX
XX CC The invention relates to a matrix comprising fibrin, a peptide which
XX CC comprises a first domain comprising a Factor XIIIa substrate and a
XX CC second domain comprising heparin or a heparin-like compound coupled to
XX CC the first domain, and a heparin binding protein (HBP), where the peptide
XX CC is covalently attached to the fibrin through the first domain. The matrix
XX CC is used for controlled release of HBP, for enhanced wound healing in
XX CC various tissues including vasculature, skin, nerve and liver. Heparin
XX CC used in the matrix protects the growth factors from proteolytic
XX CC degradation and prolong their activity until they are released from the
XX CC matrix. Despite their relatively strong affinity for heparin, heparin
XX CC binding growth factors dissociate from the matrix on a short time scale.
XX CC Therefore, high excess of binding sites is essential to ensure that they
XX CC do not diffuse far before they bind to the matrix again. This equilibrium
XX CC also allows for the binding of free growth factor to cell surface
XX CC receptors that are in close proximity to the site of dissociation. This
XX CC method of controlled release provides both relatively long term binding
XX CC of growth factors and rapid release of growth factors to local cells. The
XX CC present sequence is a peptide used to make the matrix of the invention
XX XX
XX SQ Sequence 13 AA;
XX
XX Query Match 53.7%; Score 36; DB 6; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 8.2;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX AC AAY20946;
XX XX
XX DT 22-JUL-1999 (first entry)
XX DE Human presenilin II mutant protein fragment 39.
XX XX
XX KM Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
XX KM frameshift mutation; age-related disease; neurodegenerative disorder;
XX KM Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
XX KM Huntington's disease; multiple sclerosis; alcoholic liver disease;
XX KM diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
XX KM ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
XX KM neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
XX KM glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
XX KM bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
XX KM high mobility group protein-C; neuroendocrine specific protein A.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9845322-A2.
XX XX
XX PD 15-OCT-1998.
XX XX
XX PF 02-APR-1998; 98WO-IB000705.
XX PR 10-APR-1997; 97US-0043163P.
XX XX
XX PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX PA (UYUT-) RIJKSUNIV UTRECHT.
XX XX
XX PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX XX
XX DR WPI; 1998-609901/51.
XX DR N-PSDB; AAX75762.
XX XX
XX PT Diagnosing disease by detecting frameshift mutations in RNA or
XX PT corresponding protein mutations - used to diagnose cancer and
XX PT neurological diseases, particularly Alzheimer's disease, and also for
XX PT treatment and prevention with specific ribozymes or wild-type RNA.
XX XX
XX PS Disclosure; Fig 11; 258pp; English.
XX XX
XX CC This invention describes a novel method for the diagnosis of a disease
XX CC caused by, or associated with, an RNA molecule that has a frameshift
XX CC mutation. The method is used to diagnose age-related diseases, especially
XX CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
XX CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II
XX CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
XX CC and many others listed) or susceptibility to these disorders. The method
XX CC allows a definitive diagnosis of Alzheimer's disease in living patients,
XX CC at an early stage. It is based on the observation that disease may be
XX CC caused by mutations in RNA rather than DNA. The invention describes the
XX CC use of neuronal system RNA molecules, specifically proteins including
XX CC beta-amyloid precursor protein (beta-APP), the microtubule associated
XX CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
XX CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
XX CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
XX CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
XX CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
XX CC protein-C (HMGP-C) and neuroendocrine specific protein A
XX XX
XX SQ Sequence 13 AA;
XX
XX Query Match 40.3%; Score 27; DB 2; Length 13;
XX Best Local Similarity 44.4%; Pred. No. 4.1e+02;
XX Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 10
 AAY20946
 ID AAY20946 standard; protein; 13 AA.

RESULT 11
AAV20420
ID AAV20420 standard; protein; 13 AA.
XX
XX AAV20420;
AC
XX 22-JUL-1999 (first entry)
XX
XX Human microtubule associated protein 2 mutant fragment 116.
DE
XX Human; beta-amyloid precursor protein; beta-ApP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGp-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9845322-A2.
XX
XX 15-OCT-1998.
XX
XX 02-APR-1998; 98WO-IB000705.
XX
XX 10-APR-1997; 97US-0043163P.
XX
XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
XX (UYUT-) RIJKSONIV UTRECHT.
XX
XX Van Leeuwen FW, Grosveld FG, Burbach JPH;
PI
XX WPI: 1998-609901/51.
XX N-PSDB; AAX75757.
XX
XX
XX Diagnosing disease by detecting frameshift mutations in RNA or
XX corresponding protein mutations - used to diagnose cancer and
XX neurological diseases, particularly Alzheimer's disease, and also for
XX treatment and prevention with specific ribozymes or wild-type RNA.
XX
XX
XX Disclosure; Fig 6; 258pp; English.
XX
XX This invention describes a novel method for the diagnosis of a disease
XX caused by, or associated with, an RNA molecule that has a frameshift
XX mutation. The method is used to diagnose age-related diseases, especially
XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
XX and many others listed) or susceptibility to these disorders. The method
XX allows a definitive diagnosis of Alzheimer's disease in living patients,
XX at an early stage. It is based on the observation that disease may be
XX caused by mutations in RNA rather than DNA. The invention describes the
XX use of neuronal system RNA molecules, specifically proteins including
XX beta-amyloid precursor protein (beta-ApP), the microtubule associated
XX proteins tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
XX neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
XX 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
XX protein-C (HMGp-C) and neuroendocrine specific protein A
XX
XX Sequence 13 AA;

Query Match 38.8%; Score 26; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DEQVSP 7
||:|
Db 3 QREISP 8

RESULT 12
AAR54972
ID AAR54972 standard; peptide; 13 AA.
XX
XX AAR54972;
AC
XX 25-MAR-2003 (revised)
XX 31-OCT-1994 (first entry)
XX
XX Sorhi grass pollen allergen T cell epitope.
DE
XX IGE; allergy; antigen; diagnosis; treatment; Group I allergen.
KW
XX Sorghum halepense.
OS
XX
XX WO9410314-A1.
XX
XX 11-MAY-1994.
XX
XX 29-OCT-1993; 93WO-AU000559.
XX
XX 30-OCT-1992; 92US-00971096.
XX
XX (UYME) UNIV MELBOURNE.
XX
XX Singh MB, Knox RB, Avijoojlu A;
XX
XX WPI: 1994-167469/20.
XX
XX
XX DNA encoding allergenic proteins and peptide(s) from Johnson grass pollen
XX allergen Sorhi - for diagnosing, treating and preventing allergy to
XX Johnson pollen.
XX
XX
XX Claim 20; Fig 9; 81pp; English.
XX
XX
XX The sequence is that of a Sorhi Group I grass pollen allergen T cell
XX epitope corresp. to residues 93-105 of Sorhi clone 35. See also AAR54949-
XX 76. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 13 AA;

Query Match 37.3%; Score 25; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NOEQVSPY 8
||:|
Db 4 NYEQIAAY 11

RESULT 13
AAM38008
ID AAM38008 standard; peptide; 13 AA.
XX
XX AAM38008;
AC
XX 23-APR-1998 (first entry)
XX
XX WW domain binding clone 4 obtained from a pp library.
DE
XX Peptide recognition unit; WW domain; cell signalling; growth regulation;
KW cytoskeleton organisation; targeted drug screening; modulator;
KW WW domain interaction.
XX
XX Synthetic.
OS

Query Match 38.8%; Score 26; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;

```

FH Key Location/Qualifiers
FT Region 6..9
XX /note= "PPPPY motif"
XX
XX WO9737223-A1.
XX
XX 09-OCT-1997.
XX
XX 03-APR-1997; 97WO-US005547.
XX
XX 03-APR-1996; 96US-00630916.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UNNC-) UNIV NORTH CAROLINA.
XX
XX Pirozzi G, Kay BK, Fowlkes DM;
XX
XX WPI, 1997-503234/46.
XX
XX Identifying cell signalling and growth regulatory polypeptides by
XX reaction with multivalent recognition complex - polypeptides are useful
XX in targeted drug selection.
XX
XX Claim 92; Fig 27; 220pp; English.
XX
XX Peptides AAW38005-08 are the sequences of WW domain binding clones
XX obtained by screening random or biased libraries with the WW domains of
XX the novel WWP proteins. The present peptide was obtained after screening
XX with WW domain 1 of WWP1 (WWP1.1). The peptides are peptide recognition
XX units ("ligands"), and are used for analysing specificities of the WW
XX domains. The WW domain is a small functional domain. Its name is derived
XX from the observation that two tryptophan residues, one in the amino
XX terminal portion of the WW domain and one in the carboxyl terminal
XX portion, are conserved. Most proteins containing WW domains have a
XX function involving cell signalling and growth regulation or the
XX organisation of the cytoskeleton. Polypeptides containing a WW domain are
XX identified by treating a multivalent recognition unit complex that has
XX selective binding affinity for a WW domain, with many polypeptides and
XX identifying those with selective affinity for the complex. Proteins
XX containing WW domains are used for targeted drug screening, i.e. to
XX identify potential modulators of specific WW domain interactions. note:
XX sequence in SEQ ID listing differs from sequence given in figure. The SEQ
XX ID sequence is as follows: GPSRQPPPYRYTVK
XX
XX Sequence 13 AA;
XX
XX Query Match 37.3%; Score 25; DB 2; Length 13;
XX Best Local Similarity 50.0%; Pred. No. 9.8e+02;
XX Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 3 EQVSPYTLK 12
XX |||||
XX 4 EQPPYRYTVK 13
XX
XX RESULT 14
XX AAE23145
XX ID AAE23145 standard; peptide; 13 AA.
XX
XX AAE23145;
XX
XX 21-AUG-2002 (first entry)
XX
XX Influenza A virus subtype 16 haemagglutinin (HA) protein fragment #9.
XX
XX Haemagglutinin; HA protein; vaccine; infection.
XX
XX Influenza A virus.
XX
XX WC200224734-A2.
XX
XX 28-MAR-2002.
XX

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PF 19-SEP-2001; 2001WO-IB001914.
XX
XX 19-SEP-2000; 2000GB-00022969.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Fouchier R, Olsen B, Osterhaus A;
XX
XX WPI, 2002-416272/44.
XX
XX
XX New isolated protein of influenza A virus subtype H16 useful for
XX preparing vaccines for treating influenza A virus infection, and for
XX detecting influenza virus in a sample.
XX
XX Claim 4; Page 57; 59pp; English.
XX
XX The invention relates to influenza A virus subtype (designated H16)
XX haemagglutinin (HA) proteins and nucleic acid encoding such proteins.
XX Sequences of the invention are useful as vaccines. They are also used in
XX the manufacture of a medicament for treating or preventing influenza A
XX virus infections. The present sequence is influenza A virus subtype H16
XX HA protein fragment
XX
XX Sequence 13 AA;
XX
XX Query Match 37.3%; Score 25; DB 5; Length 13;
XX Best Local Similarity 66.7%; Pred. No. 9.8e+02;
XX Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 SPYTL 11
XX :|||||
XX Db 2 NPYTLV 7
XX
XX RESULT 15
XX AAR34779
XX ID AAR34779 standard; peptide; 13 AA.
XX
XX AAR34779;
XX
XX 25-MAR-2003 (revised)
XX 16-JUL-1993 (first entry)
XX
XX CAD tryptic peptide, internal sequence 10.
XX
XX Tobacco; cinamy1 alcohol dehydrogenase; CAD; tryptic peptide; subunit;
XX probe; primer; plant; lignin; biosynthesis; biosynthesis; digestibility;
XX feed; cellulose; crop; pathogen; timber.
XX
XX Nicotiana tabacum.
XX
XX WO9305159-A1.
XX
XX 18-MAR-1993.
XX
XX 27-APR-1992; 92WO-GB000774.
XX
XX 26-APR-1991; 91GB-00009063.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Boudet AM, Inze DG, Schuch WW;
XX
XX WPI, 1993-100982/12.
XX
XX Modifying lignin content of plants - comprises use of recombinant DNA
XX encoding lignin biosynthesis enzyme, e.g. CAD.
XX
XX Disclosure; Fig 1; 69pp; English.
XX
XX The sequences given in AAR34768-82 represent peptide sequences derived
XX from tobacco cinamy1 alcohol dehydrogenase (CAD) tryptic peptides.
XX Purified CAD consists of two subunits of approximate molecular weights
XX

```

CC 42.5 kD and 44 kD. These peptides were derived by trypsin digestion of
CC both polypeptides. These peptides were used to produce probes and primers
CC which were used in the isolation of the CAD cDNA. The CAD cDNA may be
CC used in the production of a recombinant DNA comprising a gene which is
CC essential to plant lignin biosynthesis. When incorporated into a plant
CC genome by transformation, mRNA transcribed from the coding region
CC inhibits production of the enzyme from the endogenous gene. The
CC recombinant DNA may be used to provide plants having altered ability to
CC synthesise lignin. The principle applications of altered lignin
CC biosynthesis are improvement of digestibility of animal forage crops,
CC reduction of lignin in woody feedstocks for cellulose fibre extraction,
CC improvement of the response of crop plants to pathogen attack and
CC improvement of timber quality. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX

SQ Sequence 13 AA;

Query Match 35.8%; Score 24; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VSPYT 9
:||||
Db 5 LSPYT 9

Search completed: October 1, 2004, 13:47:59
Job time : 54 secs